

SEP 23 2003

TECH CENT



1600

## RAW SEQUENCE LISTING

DATE: 09/15/2003

PATENT APPLICATION: US/09/964,858A

TIME: 15:33:45

Input Set : A:\sequencelisting\_09-964,858.txt

Output Set: N:\CRF4\09152003\I964858A.raw

3 <110> APPLICANT: HOSTETTER, Margaret K.  
 4 DEVORE-CARTER, Denise  
 6 <120> TITLE OF INVENTION: ANTIBODIES TO THE PROPEPTIDE OF CANDIDA ALBICANS  
 8 <130> FILE REFERENCE: P07274US02/BAS  
 10 <140> CURRENT APPLICATION NUMBER: US 09/964,858A  
 11 <141> CURRENT FILING DATE: 2001-09-28  
 13 <150> PRIOR APPLICATION NUMBER: US 60/237,082  
 14 <151> PRIOR FILING DATE: 2000-09-28  
 16 <160> NUMBER OF SEQ ID NOS: 8  
 18 <170> SOFTWARE: PatentIn version 3.1  
 20 <210> SEQ ID NO: 1  
 21 <211> LENGTH: 1664  
 22 <212> TYPE: PRT  
 23 <213> ORGANISM: Candida albicans  
 25 <400> SEQUENCE: 1  
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 28 1 5 10 15  
 31 Leu Gln Leu Gln Pro Gln Ser Ser Ser Ala Ser Ile Phe Asn Ser Pro  
 32 20 25 30  
 35 Thr Lys Pro Leu Asn Phe Pro Arg Thr Asn Ser Lys Pro Ser Leu Asp  
 36 35 40 45  
 39 Pro Asn Ser Ser Ser Asp Thr Tyr Thr Ser Glu Gln Asp Gln Glu Lys  
 40 50 55 60  
 43 Gly Lys Glu Glu Lys Lys Asp Thr Ala Phe Gln Thr Ser Phe Asp Arg  
 44 65 70 75 80  
 47 Asn Phe Asp Leu Asp Asn Ser Ile Asp Ile Gln Gln Thr Ile Gln His  
 48 85 90 95  
 51 Gln Gln Gln Gln Pro Gln Gln Gln Gln Leu Ser Gln Thr Asp Asn  
 52 100 105 110  
 55 Asn Leu Ile Asp Glu Phe Ser Phe Gln Thr Pro Met Thr Ser Thr Leu  
 56 115 120 125  
 59 Asp Leu Thr Lys Gln Asn Pro Thr Val Asp Lys Val Asn Glu Asn His  
 60 130 135 140  
 63 Ala Pro Thr Tyr Ile Asn Thr Ser Pro Asn Lys Ser Ile Met Lys Lys  
 64 145 150 155 160  
 67 Ala Thr Pro Lys Ala Ser Pro Lys Lys Val Ala Phe Thr Val Thr Asn  
 68 165 170 175  
 71 Pro Glu Ile His His Tyr Pro Asp Asn Arg Val Glu Glu Glu Asp Gln  
 72 180 185 190  
 75 Ser Gln Gln Lys Glu Asp Ser Val Glu Pro Pro Leu Ile Gln His Gln  
 76 195 200 205  
 79 Trp Lys Asp Pro Ser Gln Phe Asn Tyr Ser Asp Glu Asp Thr Asn Ala  
 80 210 215 220

ENTERED

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83 Ser Val Pro Pro Thr Pro Pro Leu His Thr Thr Lys Pro Thr Phe Ala
84 225                230                235                240
87 Gln Leu Leu Asn Lys Asn Asn Glu Val Asn Ser Glu Pro Glu Ala Leu
88                245                250                255
91 Thr Asp Met Lys Leu Lys Arg Glu Asn Phe Ser Asn Leu Ser Leu Asp
92                260                265                270
95 Glu Lys Val Asn Leu Tyr Leu Ser Pro Thr Asn Asn Asn Ser Lys
96                275                280                285
99 Asn Val Ser Asp Met Asp Ser His Leu Gln Asn Leu Gln Asp Ala Ser
100                290                295                300
103 Lys Asn Lys Thr Asn Glu Asn Ile His Asn Leu Ser Phe Ala Leu Lys
104 305                310                315                320
107 Ala Pro Lys Asn Asp Ile Glu Asn Pro Leu Asn Ser Leu Thr Asn Ala
108                325                330                335
111 Asp Ile Ser Leu Arg Ser Ser Gly Ser Ser Gln Ser Ser Leu Gln Ser
112                340                345                350
115 Leu Arg Asn Asp Asn Arg Val Leu Glu Ser Val Pro Gly Ser Pro Lys
116                355                360                365
119 Lys Val Asn Pro Gly Leu Ser Leu Asn Asp Gly Ile Lys Gly Phe Ser
120                370                375                380
123 Asp Glu Val Val Glu Ser Leu Leu Pro Arg Asp Leu Ser Arg Asp Lys
124 385                390                395                400
127 Leu Glu Thr Thr Lys Glu His Asp Ala Pro Glu His Asn Asn Glu Asn
128                405                410                415
131 Phe Ile Asp Ala Lys Ser Thr Asn Thr Asn Lys Gly Gln Leu Leu Val
132                420                425                430
135 Ser Ser Asp Asp His Leu Asp Ser Phe Asp Arg Ser Tyr Asn His Thr
136                435                440                445
139 Glu Gln Ser Ile Leu Asn Leu Leu Asn Ser Ala Ser Gln Ser Gln Ile
140                450                455                460
143 Ser Leu Asn Ala Leu Glu Lys Gln Arg Gln Thr Gln Glu Gln Glu Gln
144 465                470                475                480
147 Thr Gln Ala Ala Glu Pro Glu Glu Glu Thr Ser Phe Ser Asp Asn Ile
148                485                490                495
151 Lys Val Lys Gln Glu Pro Lys Ser Asn Leu Glu Phe Val Lys Val Thr
152                500                505                510
155 Ile Lys Lys Glu Pro Val Ser Ala Thr Glu Ile Lys Ala Pro Lys Arg
156                515                520                525
159 Glu Phe Ser Ser Arg Ile Leu Arg Ile Lys Asn Glu Asp Glu Ile Ala
160                530                535                540
163 Glu Pro Ala Asp Ile His Pro Lys Lys Glu Asn Glu Ala Asn Ser His
164 545                550                555                560
167 Val Glu Asp Thr Asp Ala Leu Leu Lys Lys Ala Leu Asn Asp Asp Glu
168                565                570                575
171 Glu Ser Asp Thr Thr Gln Asn Ser Thr Lys Met Ser Ile Arg Phe His
172                580                585                590
175 Ile Asp Ser Asp Trp Lys Leu Glu Asp Ser Asn Asp Gly Asp Arg Glu
176                595                600                605
179 Asp Asn Asp Asp Ile Ser Arg Phe Glu Lys Ser Asp Ile Leu Asn Asp

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180      610      615      620
183 Val Ser Gln Thr Ser Asp Ile Ile Gly Asp Lys Tyr Gly Asn Ser Ser
184 625      630      635      640
187 Ser Glu Ile Thr Thr Lys Thr Leu Ala Pro Arg Ser Asp Asn Asn
188      645      650      655
191 Asp Lys Glu Asn Ser Lys Ser Leu Glu Asp Pro Ala Asn Asn Glu Ser
192      660      665      670
195 Leu Gln Gln Gln Leu Glu Val Pro His Thr Lys Glu Asp Asp Ser Ile
196      675      680      685
199 Leu Ala Asn Ser Ser Asn Ile Ala Pro Pro Glu Glu Leu Thr Leu Pro
200      690      695      700
203 Val Val Glu Ala Asn Asp Tyr Ser Ser Phe Asn Asp Val Thr Lys Thr
204 705      710      715      720
207 Phe Asp Ala Tyr Ser Ser Phe Glu Glu Ser Leu Ser Arg Glu His Glu
208      725      730      735
211 Thr Asp Ser Lys Pro Ile Asn Phe Ile Ser Ile Trp His Lys Gln Glu
212      740      745      750
215 Lys Gln Lys Lys His Gln Ile His Lys Val Pro Thr Lys Gln Ile Ile
216      755      760      765
219 Ala Ser Tyr Gln Gln Tyr Lys Asn Glu Gln Glu Ser Arg Val Thr Ser
220      770      775      780
223 Asp Lys Val Lys Ile Pro Asn Ala Ile Gln Phe Lys Lys Phe Lys Glu
224 785      790      795      800
227 Val Asn Val Met Ser Arg Arg Val Val Ser Pro Asp Met Asp Asp Leu
228      805      810      815
231 Asn Val Ser Gln Phe Leu Pro Glu Leu Ser Glu Asp Ser Gly Phe Lys
232      820      825      830
235 Asp Leu Asn Phe Ala Asn Tyr Ser Asn Asn Thr Asn Arg Pro Arg Ser
236      835      840      845
239 Phe Thr Pro Leu Ser Thr Lys Asn Val Leu Ser Asn Ile Asp Asn Asp
240      850      855      860
243 Pro Asn Val Val Glu Pro Pro Glu Pro Lys Ser Tyr Ala Glu Ile Arg
244 865      870      875      880
247 Asn Ala Arg Arg Leu Ser Ala Asn Lys Ala Ala Pro Asn Gln Ala Pro
248      885      890      895
251 Pro Leu Pro Pro Gln Arg Gln Pro Ser Ser Thr Arg Ser Asn Ser Asn
252      900      905      910
255 Lys Arg Val Ser Arg Phe Arg Val Pro Thr Phe Glu Ile Arg Arg Thr
256      915      920      925
259 Ser Ser Ala Leu Ala Pro Cys Asp Met Tyr Asn Asp Ile Phe Asp Asp
260      930      935      940
263 Phe Gly Ala Gly Ser Lys Pro Thr Ile Lys Ala Glu Gly Met Lys Thr
264 945      950      955      960
267 Leu Pro Ser Met Asp Lys Asp Asp Val Lys Arg Ile Leu Asn Ala Lys
268      965      970      975
271 Lys Gly Val Thr Gln Asp Glu Tyr Ile Asn Ala Lys Leu Val Asp Gln
272      980      985      990
275 Lys Pro Lys Lys Asn Ser Ile Val Thr Asp Pro Glu Asp Arg Tyr Glu
276      995      1000      1005

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279	Glu	Leu	Gln	Gln	Thr	Ala	Ser	Ile	His	Asn	Ala	Thr	Ile	Asp	Ser
280		1010					1015					1020			
283	Ser	Ile	Tyr	Gly	Arg	Pro	Asp	Ser	Ile	Ser	Thr	Asp	Met	Leu	Pro
284		1025					1030					1035			
287	Tyr	Leu	Ser	Asp	Glu	Leu	Lys	Lys	Pro	Pro	Thr	Ala	Leu	Leu	Ser
288		1040					1045					1050			
291	Ala	Asp	Arg	Leu	Phe	Met	Glu	Gln	Glu	Val	His	Pro	Leu	Arg	Ser
292		1055					1060					1065			
295	Asn	Ser	Val	Leu	Val	His	Pro	Gly	Ala	Gly	Ala	Ala	Thr	Asn	Ser
296		1070					1075					1080			
299	Ser	Met	Leu	Pro	Glu	Pro	Asp	Phe	Glu	Leu	Ile	Asn	Ser	Pro	Ala
300		1085					1090					1095			
303	Arg	Asn	Val	Ser	Asn	Asn	Ser	Asp	Asn	Val	Ala	Ile	Ser	Gly	Asn
304		1100					1105					1110			
307	Ala	Ser	Thr	Ile	Ser	Phe	Asn	Gln	Leu	Asp	Met	Asn	Phe	Asp	Asp
308		1115					1120					1125			
311	Gln	Ala	Thr	Ile	Gly	Gln	Lys	Ile	Gln	Glu	Gln	Pro	Ala	Ser	Lys
312		1130					1135					1140			
315	Ser	Ala	Asn	Thr	Val	Arg	Gly	Asp	Asp	Asp	Gly	Leu	Ala	Ser	Ala
316		1145					1150					1155			
319	Pro	Glu	Thr	Pro	Arg	Thr	Pro	Thr	Lys	Lys	Glu	Ser	Ile	Ser	Ser
320		1160					1165					1170			
323	Lys	Pro	Ala	Lys	Leu	Ser	Ser	Ala	Ser	Pro	Arg	Lys	Ser	Pro	Ile
324		1175					1180					1185			
327	Lys	Ile	Gly	Ser	Pro	Val	Arg	Val	Ile	Lys	Lys	Asn	Gly	Ser	Ile
328		1190					1195					1200			
331	Ala	Gly	Ile	Glu	Pro	Ile	Pro	Lys	Ala	Thr	His	Lys	Pro	Lys	Lys
332		1205					1210					1215			
335	Ser	Phe	Gln	Gly	Asn	Glu	Ile	Ser	Asn	His	Lys	Val	Arg	Asp	Gly
336		1220					1225					1230			
339	Gly	Ile	Ser	Pro	Ser	Ser	Gly	Ser	Glu	His	Gln	Gln	His	Asn	Pro
340		1235					1240					1245			
343	Ser	Met	Val	Ser	Val	Pro	Ser	Gln	Tyr	Thr	Asp	Ala	Thr	Ser	Thr
344		1250					1255					1260			
347	Val	Pro	Asp	Glu	Asn	Lys	Asp	Val	Gln	His	Lys	Pro	Arg	Glu	Lys
348		1265					1270					1275			
351	Gln	Lys	Gln	Lys	His	His	His	Arg	His	His	His	His	His	His	Lys
352		1280					1285					1290			
355	Gln	Lys	Thr	Asp	Ile	Pro	Gly	Val	Val	Asp	Asp	Glu	Ile	Pro	Asp
356		1295					1300					1305			
359	Val	Gly	Leu	Gln	Glu	Arg	Gly	Lys	Leu	Phe	Phe	Arg	Val	Leu	Gly
360		1310					1315					1320			
363	Ile	Lys	Asn	Ile	Asn	Leu	Pro	Asp	Ile	Asn	Thr	His	Lys	Gly	Arg
364		1325					1330					1335			
367	Phe	Thr	Leu	Thr	Leu	Asp	Asn	Gly	Val	His	Cys	Val	Thr	Thr	Pro
368		1340					1345					1350			
371	Glu	Tyr	Asn	Met	Asp	Asp	His	Asn	Val	Ala	Ile	Gly	Lys	Glu	Phe
372		1355					1360					1365			
375	Glu	Leu	Thr	Val	Ala	Asp	Ser	Leu	Glu	Phe	Ile	Leu	Thr	Leu	Lys

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376      1370      1375      1380
379 Ala Ser Tyr Glu Lys Pro Arg Gly Thr Leu Val Glu Val Thr Glu
380      1385      1390      1395
383 Lys Lys Val Val Lys Ser Arg Asn Arg Leu Ser Arg Leu Phe Gly
384      1400      1405      1410
387 Ser Lys Asp Ile Ile Thr Thr Thr Lys Phe Val Pro Thr Glu Val
388      1415      1420      1425
391 Lys Asp Thr Trp Ala Asn Lys Phe Ala Pro Asp Gly Ser Phe Ala
392      1430      1435      1440
395 Arg Cys Tyr Ile Asp Leu Gln Gln Phe Glu Asp Gln Ile Thr Gly
396      1445      1450      1455
399 Lys Ala Ser Gln Phe Asp Leu Asn Cys Phe Asn Glu Trp Glu Thr
400      1460      1465      1470
403 Met Ser Asn Gly Asn Gln Pro Met Lys Arg Gly Lys Pro Tyr Lys
404      1475      1480      1485
407 Ile Ala Gln Leu Glu Val Lys Met Leu Tyr Val Pro Arg Ser Asp
408      1490      1495      1500
411 Pro Arg Glu Ile Leu Pro Thr Ser Ile Arg Ser Ala Tyr Glu Ser
412      1505      1510      1515
415 Ile Asn Glu Leu Asn Asn Glu Gln Asn Asn Tyr Phe Glu Gly Tyr
416      1520      1525      1530
419 Leu His Gln Glu Gly Gly Asp Cys Pro Ile Phe Lys Lys Arg Phe
420      1535      1540      1545
423 Phe Lys Leu Met Gly Thr Ser Leu Leu Ala His Ser Glu Ile Ser
424      1550      1555      1560
427 His Lys Thr Arg Ala Lys Ile Asn Leu Ser Lys Val Val Asp Leu
428      1565      1570      1575
431 Ile Tyr Val Asp Lys Glu Asn Ile Asp Arg Ser Asn His Arg Asn
432      1580      1585      1590
435 Phe Ser Asp Val Leu Leu Leu Asp His Ala Phe Lys Ile Lys Phe
436      1595      1600      1605
439 Ala Asn Gly Glu Leu Ile Asp Phe Cys Ala Pro Asn Lys His Glu
440      1610      1615      1620
443 Met Lys Ile Trp Ile Gln Asn Leu Gln Glu Ile Ile Tyr Arg Asn
444      1625      1630      1635
447 Arg Phe Arg Arg Gln Pro Trp Val Asn Leu Met Leu Gln Gln Gln
448      1640      1645      1650
451 Gln Gln Gln Gln Gln Gln Gln Ser Ser Gln Gln
452      1655      1660
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456 <211> LENGTH: 5194
457 <212> TYPE: DNA
458 <213> ORGANISM: Candida albicans
460 <400> SEQUENCE: 2
461 cccaaaaaag ataaaataaa aacaaaacaa aacaaaagta ctaacaaatt attgaaactt      60
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465 aaattattac cgatagataa acattctcat ttacaattac agcctcaatc gtcctcgga      180
467 tcaatattta attccccaac aaaaccattg aatttcccca gaacaaattc caagccgagt      240
469 ttagatccaa attcaagctc tgatacctac actagcgaac aagatcaaga gaaagggaaa      300

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VERIFICATION SUMMARY

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